

LOCUS	AF186371	3014 bp	DNA	linear	BCT 10-SEP-2002
DEFINITION	Streptomyces coelicolor A3(2) AhpD (ahpD), AhpC (ahpC), and OxyR (oxyR) genes, complete cds.				
ACCESSION	AF186371				
VERSION	AF186371.1 GI:6288864				
SOURCE	Streptomyces coelicolor A3(2)				
ORGANISM	Streptomyces coelicolor A3(2) Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.				
REFERENCE	1 (bases 1 to 3014)				
AUTHORS	Hahn,J.S., Oh,S.Y. and Roe,J.H.				
TITLE	Role of OxyR as a Peroxide-Sensing Positive Regulator in Streptomyces coelicolor A3(2)				
JOURNAL	J. Bacteriol. 184 (19), 5214-5222 (2002)				
MEDLINE	22206464				
PUBMED	12218006				
REFERENCE	2 (bases 1 to 3014)				
AUTHORS	Hahn,J.-S. and Roe,J.-H.				
TITLE	Role of OxyR as a regulator of the ahpCD operon encoding alkyl hydroperoxide reductase system in Streptomyces coelicolor				
JOURNAL	Unpublished				
REFERENCE	3 (bases 1 to 3014)				
AUTHORS	Hahn,J.-S. and Roe,J.-H.				
TITLE	Direct Submission				
JOURNAL	Submitted (15-SEP-1999) Microbiology, Seoul National University, Kwan-Ak Gu, Shin-Lim 9Dong, San 56-1, Seoul 151-742, Korea				

Query Match 13.0%; Score 217.2; DB 1; Length 3014;
Best Local Similarity 53.6%; Pred. No. 2.8e-43;
Matches 478; Conservative 0; Mismatches 408; Indels 6; Gaps 1;

[illegible]

Db 2186 ACGAGCGCTATCCCGACCTCGACCTCCAGGTCCACGAGGAGCAGACGGCGAGCCTCCTGG 2245
 Qy 912 CGTTGCTGCGCGACGGCGCCATCGACGTCGCCATGATGGCCCTGCCTTCTGAGGCACCAG 971
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2246 AGGGCCTGACGACCGGCCGGCTCGACCTGCTGCTGCTCGCGGTGCCCTCGGCGTCCCCG 2305
 Qy 972 GCATGAAGGAAATCCCCCTCTACGACGAAGACTTTATCGTCGTTACAGCTAGCGATCACC 1031
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2306 GCGTCACCGAACTCCCGCTCTTCGACGAGGACTTCGTCCTGGTCACGCCGCTCGACCACC 2365
 Qy 1032 CCTTCGCCGGCCGCCAAGACTTAGAACTATCCGCCTTAGAAGACCTCGATCTGCTGCTTC 1091
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2366 GACTCGGCGGCCGGGAGGGCCTGGAGCGCTCGGTGCTGCGCGAGCTGAAGCTGCTGCTGC 2425
 Qy 1092 TCGACGACGGACACTGCCTCCACGACCAAATTGTGGACCTGTGCCGCCGCGGAGACATCA 1151
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2426 TCGACGAGGGGCACTGCCTGCGCGACCAGGCGCTCGACATCTGCC-----GGGAGGCGG 2479
 Qy 1152 ACCCCATTAGCTCCACTACTGCTGTCACCCGCGCATCCAGCCTTACCACCGTCATGCAGC 1211
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2480 GCCGCGCGGGGTCCCGGCGACGACGACCACGGCCGCCGGTCTGTGACGCTGGTACAGC 2539
 Qy 1212 TCGTCGTCGCCGGCCTTGGATCCACCTTGGTCCCAATCAGCGCAATCCCATGGGAATGCA 1271
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2540 TGGTGGCGGGCGGCCTCGGGGTGACGCTGCTGCCCCGCACCGCCGTCCGGGTGGAGACCT 2599
 Qy 1272 CCCGACCAGGACTGGCAACAGCCAACTTCAACTCTGATGTCACCGCAAACCGCCGCATTG 1331
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2600 CCCGCTCCAGCCAGCTCCTCACC CGTCCTTACCGACCGGCCCCCACC CGCGTATCG 2659
 Qy 1332 GATTGGTGTACCGTTCCTCTTCTTCGCGCCGAAGAGTTCGAACAGTTTGC 1383
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2660 CCCTCGCCATGCGCACGGGCGCGGCCCGCTCGGCGGAGTACGGGGAAGTGGC 2711